

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 09/545, 199B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics**  
     **Wrapped Aminos**    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2 ☐ **Invalid Line Length**    The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3 ☐ **Misaligned Amino Numbering**    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
  
- 4 ☐ **Non-ASCII**    The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
  
- 5 ☐ **Variable Length**    Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6 ☐ **PatentIn 2.0 "bug"**    A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7 ☐ **Skipped Sequences (OLD RULES)**    Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
     (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
     (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
     (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
     This sequence is intentionally skipped  
  
     Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8 ☐ **Skipped Sequences (NEW RULES)**    Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
     <210> sequence id number  
     <400> sequence id number  
     000
  
- 9 ☒ **Use of n's or Xaa's (NEW RULES)**    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
     In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10 ☐ **Invalid <213> Response**    Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
  
- 11 ☐ **Use of <220>**    Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
     (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12 ☒ **PatentIn 2.0 "bug"**    Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

1643

## RAW SEQUENCE LISTING

DATE: 06/27/2001

PATENT APPLICATION: US/09/545,199B

TIME: 12:40:15

Input Set : C:\Crf3\Datahold\09545199

Output Set: N:\CRF3\06262001\I545199B.raw

Does Not Comply  
Corrected Diskette Needed

C--&gt; 2 &lt;140&gt; CURRENT APPLICATION NUMBER: US/09/545,199B

C--&gt; 2 &lt;141&gt; CURRENT FILING DATE: 2000-04-06

W--&gt; 2 &lt;151&gt; PRIOR FILING DATE: 1999-09-10

W--&gt; 0 &lt;110&gt; APPLICANT:

W--&gt; 0 &lt;120&gt; TITLE INVENTION:

W--&gt; 0 &lt;130&gt; FILE REFERENCE:

4 &lt;150&gt; PRIOR APPLICATION NUMBER: 60/128,689

5 &lt;151&gt; PRIOR FILING DATE: 1999-04-09

7 &lt;160&gt; NUMBER OF SEQ ID NOS: 165

9 &lt;170&gt; SOFTWARE: PatentIn Ver. 2.0

*These mandatory features  
are missing from file.  
Possible PatentIn 2.0 "bug".  
See #12 on the Error  
Summary Sheet.*

## ERRORED SEQUENCES

1952 &lt;210&gt; SEQ ID NO: 16

1953 &lt;211&gt; LENGTH: 2110

1954 &lt;212&gt; TYPE: PRT

1955 &lt;213&gt; ORGANISM: Pasteurella multocida

1957 &lt;400&gt; SEQUENCE: 16

1958 Met Gln Pro Ala Gln Glu His Cys Gln Arg Ile Asn Asn Ile Val Asn

1959 1 5 10 15

1961 Gln Glu Asn Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala

1962 20 25 30

1964 Glu Arg Ser Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu

1965 35 40 45

1967 Thr Val His Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn

1968 50 55 60

1970 Val Ser Tyr Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg

1971 65 70 75 80

1973 Val Ala Val His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn

1974 85 90 95

1976 Leu Gln Glu Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala

1977 100 105 110

1979 Ile Arg Ser Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser

1980 115 120 125

1982 Ser Glu Ser Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys

1983 130 135 140

1985 Gly Thr Phe Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala

1986 145 150 155 160

1988 Phe Asn Gln Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile

1989 165 170 175

1991 Thr Met Tyr Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser

1992 180 185 190

1994 Gly Asn Ala Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala

1995 195 200 205

1997 Leu Phe Gly Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu

1998 210 215 220

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Input Set : C:\Crf3\Datahold\09545199

Output Set: N:\CRF3\06262001\I545199B.raw

```

2000 Asn Phe Ser Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met
2001 225                230                235                240
2003 Tyr Gln Lys Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys
2004                245                250                255
2006 Ser Tyr Asp Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro
2007                260                265                270
2009 Thr Asp Phe Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly
2010                275                280                285
2012 Lys Leu Glu Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu
2013                290                295                300
2015 Arg Gly Lys Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser
2016 305                310                315                320
2018 Leu Pro Ser Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu
2019                325                330                335
2021 Glu Glu Asp Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met
2022                340                345                350
2024 Pro Asn Leu Phe Ile Asp Asn Ser Ser Ile Gln Leu Glu Lys Lys Lys Leu
2025                355                360                365
2027 Ser Pro Ile Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile
2028                370                375                380
2030 Glu Glu Ser His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp
2031 385                390                395                400
2033 Asp Glu Ser Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu
2034                405                410                415
2036 Lys Glu Met Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly
2037                420                425                430
2039 Asn Lys Pro Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp
2040                435                440                445
2042 Glu Phe Phe Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu
2043                450                455                460
2045 Gly Glu Glu Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser
2046 465                470                475                480
2048 Thr Asn Leu Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys
2049                485                490                495
2051 Arg Glu Lys Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys
2052                500                505                510
2054 Leu Gln Glu Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln
2055                515                520                525
2057 Lys Ala Arg Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu
2058                530                535                540
2060 Lys Arg Val Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp
2061 545                550                555                560
2063 Lys Ile Ala Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu
2064                565                570                575
2066 Glu Ile Arg Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu
2067                580                585                590
2069 Glu Lys Lys Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln
2070                595                600                605
2072 Ala Glu Gln Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu

```

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2073	610					615				620						
2075	Asp	Ile	Glu	Gln	Gln	Lys	Ala	Tyr	Glu	Glu	Met	Ala	Lys	Arg	Glu	Ala
2076	625					630				635					640	
2078	Glu	Ala	Ser	Lys	Asn	Val	Leu	Leu	Lys	Ala	Ile	Asp	Glu	Glu	Arg	Pro
2079					645					650					655	
2081	Lys	Val	Glu	Thr	Asp	Pro	Leu	Phe	Arg	Thr	Lys	Leu	Lys	Tyr	Ile	Asn
2082				660					665					670		
2084	Gln	Asp	Asp	Tyr	Ala	Gly	Ala	Asn	Tyr	Phe	Phe	Asn	Lys	Val	Gly	Leu
2085			675					680				685				
2087	Asn	Thr	Lys	Gly	His	Gln	Lys	Val	Asn	Val	Leu	Gly	Asp	Asn	Tyr	Phe
2088		690					695				700					
2090	Asp	His	Gln	Val	Ile	Thr	Arg	Ser	Ile	Glu	Lys	Lys	Val	Asp	Asn	His
2091	705					710				715					720	
2093	Leu	Asn	Gln	Lys	Tyr	Asn	Leu	Ser	Asp	Val	Glu	Leu	Val	Lys	Gln	Leu
2094				725					730						735	
2096	Met	Asp	Asn	Ser	Thr	Thr	Gln	Ala	Gln	Glu	Leu	Asp	Leu	Lys	Leu	Gly
2097			740						745				750			
2099	Ala	Ala	Leu	Thr	Lys	Glu	Gln	Gln	Ala	Asn	Leu	Thr	Gln	Asp	Ile	Val
2100			755				760					765				
2102	Trp	Tyr	Val	Lys	Thr	Lys	Val	Lys	Gly	Lys	Asp	Val	Phe	Val	Pro	Lys
2103		770				775					780					
2105	Val	Tyr	Phe	Ala	Ser	Glu	Thr	Leu	Val	Glu	Ala	Gln	Lys	Leu	Gln	Gly
2106	785					790				795					800	
2108	Leu	Gly	Thr	Gly	Thr	Ile	Arg	Val	Gly	Glu	Ala	Lys	Ile	Lys	Ala	Lys
2109				805					810					815		
2111	Asp	Val	Val	Asn	Thr	Gly	Thr	Leu	Ala	Gly	Arg	Lys	Leu	Asn	Val	Glu
2112				820					825				830			
2114	Ala	Ser	Asn	Lys	Ile	Lys	Asn	Gln	Gly	Ser	Ile	Leu	Ser	Thr	Gln	Glu
2115			835				840				845					
2117	Thr	Arg	Leu	Val	Gly	Arg	Lys	Gly	Ile	Glu	Asn	Val	Ser	Arg	Ser	Phe
2118		850				855				860						
2120	Ala	Asn	Asp	Glu	Leu	Gly	Val	Thr	Ala	Gln	Arg	Ser	Glu	Ile	Lys	Thr
2121	865					870				875				880		
2123	Glu	Gly	His	Leu	His	Leu	Glu	Thr	Asp	Lys	Asp	Ser	Thr	Ile	Asp	Val
2124				885					890					895		
2126	Gln	Ala	Ser	Asp	Ile	Lys	Ala	Lys	Thr	Ser	Phe	Val	Lys	Thr	Gly	Asp
2127			900					905					910			
2129	Val	Asn	Leu	Lys	Asn	Thr	Tyr	Asn	Thr	Lys	His	Ala	Tyr	Arg	Glu	Lys
2130		915					920					925				
2132	Phe	Ser	Pro	Ser	Ala	Leu	Gln	Val	Ala	Glu	Leu	Asp	Val	Ala	Gly	Leu
2133		930				935					940					
2135	Lys	Val	Pro	Leu	Leu	Gly	Val	Ser	Ser	Pro	Ser	Ser	Tyr	Ser	Glu	His
2136	945					950				955				960		
2138	Thr	Ser	Glu	Ala	Thr	Ser	Glu	Gly	Ser	Ile	Phe	Glu	Val	Gly	His	Leu
2139				965					970					975		
2141	His	Leu	Ala	Val	Asp	Arg	Asp	Val	Asn	Gln	Ala	Gly	Ser	Lys	Ile	Lys
2142			980					985					990			
2144	Ala	Lys	Tyr	Thr	Thr	Gly	Val	Val	Lys	Gly	Asn	Phe	Asn	Thr	Glu	Ala
2145			995				1000					1005				

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Input Set : C:\Crf3\Datahold\09545199

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2147 Gly Lys Asn Ile Lys His Val Glu Lys Glu Glu Tyr Ser Ser Gln Leu
2148      1010                      1015                      1020
E--> 2150 Phe Ala Ser Ala His Ala Ser Gly Gly Gly Thr Ser Val Arg Tyr Asp
      2151 025                      1030                      1035                      1040
2153 Tyr Asn Ser Gln Asp Gly Gly Asn Ala Ser Val Gly Val Pro Thr Asn
2154      1045                      1050                      1055
2156 His Thr Gly Val Gly Ala Glu Ala Gly Met Ser Phe Thr His Thr Lys
2157      1060                      1065                      1070
2159 Asp Lys Glu Thr Leu Leu Thr His Thr Asn Ser Glu Leu Gln Val Lys
2160      1075                      1080                      1085
2162 His Gly Lys Leu His Val Leu Gly Tyr Ala Asp Ile Gly Gly Val Asp
2163      1090                      1095                      1100
E--> 2165 Ile Asn Thr Lys Leu Pro Glu Asp Ala Gln Ser Lys Ala Gln Lys Glu
      2166 105                      1110                      1115                      1120
2168 Ile Ala Ala Ser Lys Pro Glu Lys Thr Glu Gln Ser Ala Gln Asp Val
2169      1125                      1130                      1135
2171 Ala Gln Ala Gln Ser Asn Ala Asn Lys Asp Lys Glu Asn Lys Ala Pro
2172      1140                      1145                      1150
2174 Glu Ile Lys Glu Leu Ser Glu Ala Glu Ile Ala Asp Leu Met Ser Glu
2175      1155                      1160                      1165
2177 Lys Ser Lys Ala Tyr Phe Asp Asp Phe Ala Glu Gln Ala Lys Lys Ala
2178      1170                      1175                      1180
E--> 2180 Pro Glu Asn Asn Arg Phe Glu Leu Ser Ala Lys Glu Ile Lys Ser Ser
      2181 185                      1190                      1195                      1200
2183 Lys Gln Lys Asp Gln Tyr Asp His Glu Ser Glu Arg Thr Thr Phe Lys
2184      1205                      1210                      1215
2186 Val Gly Pro Glu Ala Glu Ala His Ser Ala Val Ala Asp Met Val Ser
2187      1220                      1225                      1230
2189 His Leu Val Lys Glu Tyr Arg Asp Ala Gln Asn Gly Thr Lys Gln Asp
2190      1235                      1240                      1245
2192 Gly Thr Val Ala Leu Gln His Ala Ser Asp Val Leu Asn Ile Val Thr
2193      1250                      1255                      1260
E--> 2195 Gly Asp Leu Ala Gly Ser Ser Ala Lys Leu Ser Val Glu Arg Thr His
      2196 265                      1270                      1275                      1280
2198 Glu Thr Lys Arg Thr Thr Glu Thr Gly Asp Ile Val Thr Lys Ile Gly
2199      1285                      1290                      1295
2201 Gly Asn Val Thr Leu Ser Ala Arg Ser Gly Ser Val Asn Leu Lys Asn
2202      1300                      1305                      1310
2204 Val Gln Ser Asp Glu Gln Ala Asn Leu Thr Leu Arg Ala Lys Glu Asp
2205      1315                      1320                      1325
2207 Val Asn Val Leu Ser Gly Glu Lys Thr Arg Glu Thr Thr Glu Thr Val
2208      1330                      1335                      1340
E--> 2210 Ser Arg Gln Lys Leu Ser His Gly Val Asn Ala Gly Cys Ser Met Met
      2211 345                      1350                      1355                      1360
2213 Ser Gly Ala Cys Thr Ala Gly Val Ser Thr Ser Leu Glu Gly Asn Glu
2214      1365                      1370                      1375
2216 Ser Tyr Thr Ser Glu Arg Glu Thr Ala Gln Asn Asn Ser Phe Leu Lys
2217      1380                      1385                      1390
2219 Ala Arg Asn Met Lys Val Glu Ala Gly Arg Asp Phe Asn Val Val Ser

```

*misaligned  
amino acid  
numbers.  
First digit  
of number  
must be under  
the first letter  
of the amino  
acid.*

*Phe  
1025*

*Ile  
1105*

*Pro  
1185*

*Gly  
1265*

*Ser  
1345*

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PATENT APPLICATION: US/09/545,199B

TIME: 12:40:15

Input Set : C:\Cr3\Datahold\09545199

Output Set: N:\CRF3\06262001\I545199B.raw

```

2220          1395          1400          1405
2222 Ser Asn Ile Asp Ala Asp Lys Leu Asp Leu His Val Lys Gly Lys Thr
2223          1410          1415          1420
2225 Asn Val Val Ser Lys Gln Asp Thr Leu Gln Lys Val Thr His Gly Val
E--> 2226 425          1430          1435          1440
2228 Asp Tyr Asn Leu Ser Ala Gly Val Ala Leu Ser Ser Ala Thr Ile Ala
2229          1445          1450          1455
2231 Thr Pro Thr Gly Asn Val Gly Phe Gly Tyr Thr Asn Glu Thr Glu Ser
2232          1460          1465          1470
2234 Lys Arg Thr Val Asn Gln Gln Ala Gly Ile Lys Ala Asn Lys Ile Thr
2235          1475          1480          1485
2237 Gly Gln Thr His Asp Leu Asn Leu Glu Gly Gly Tyr Leu Val Ser Asn
2238          1490          1495          1500
2240 Asp Lys Asp Asn Gln Leu Lys Val Thr Gly Asp Val Thr Thr Lys Ala
E--> 2241 505          1510          1515          1520
2243 Leu His Asp Gln His Asp Lys Asp Gly Gly Thr Phe Gly Leu Ser Val
2244          1525          1530          1535
2246 Gly Ile Ser Glu Arg Gly Thr Thr Ala Phe Asn Val Arg Gly Gly Arg
2247          1540          1545          1550
2249 Ala Glu Gln Lys His Tyr Asn Ala Thr Gln Lys Ser Thr Leu Ser Gly
2250          1555          1560          1565
2252 Val Asp Thr Ser Gln Ala Asn Val Ser Gly Gln Val Asn Thr Asp Leu
2253          1570          1575          1580
2255 Thr Lys Ala Lys Ala Val Thr Arg Asp Asp Thr Tyr Ala Ser Thr Gln
E--> 2256 585          1590          1595          1600
2258 Phe Ser Phe Glu Val Ala Asp Ile Val Glu Leu Gly Gln Arg Ala Lys
2259          1605          1610          1615
2261 Asn Lys Leu Ser Ala Pro Asn Asn Asp Thr Asp Met Ala Ser Gly Ser
2262          1620          1625          1630
2264 Thr Leu Arg Ser Arg Ser Thr Thr Glu Glu Ala Asp Val Pro Thr Thr
2265          1635          1640          1645
2267 Arg Ser Arg Val Thr Asp Glu Ala Asp Ser Val Ser Val Lys Asn Pro
2268          1650          1655          1660
2270 Ile Tyr Glu Ser Ala Asp Ala Val Val Pro Thr Pro Arg Ser Arg Asn
E--> 2271 665          1670          1675          1680
2273 Val Asp Ser Thr Asp Leu Val Asp Asn Pro Leu Tyr Ala Ser Ala Thr
2274          1685          1690          1695
2276 Thr Lys Ala Asn Ile His Asp Tyr Glu Glu Ile Pro Ala Val Tyr Ser
2277          1700          1705          1710
2279 Lys Val Gly Asp Asn Asn Ala Asp Leu Val Arg His Lys Thr Ala Thr
2280          1715          1720          1725
2282 Ser Asp Glu His Leu Tyr Ala Glu Ile Asn Glu Pro Thr Tyr Ser Arg
2283          1730          1735          1740
2285 Val Gly Asp Lys Asn Ala Asp Met Arg Arg His Asn Ala Ala Gly Thr
E--> 2286 745          1750          1755          1760
2288 Thr Asp Tyr Ala Asp Val Val Gln Ala His Thr Arg Lys Ala Asp Asp
2289          1765          1770          1775
2291 Pro Leu Pro Ala Leu Pro Asn Gln Gly Lys Ala Arg Thr Val Asn Asp
2292          1780          1785          1790

```

Same error

See  
P. 4

## RAW SEQUENCE LISTING

DATE: 06/27/2001

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TIME: 12:40:15

Input Set : C:\Crff3\Datahold\09545199

Output Set: N:\CRF3\06262001\I545199B.raw

2294 Gly Ser Glu His Ile Tyr Thr Asp Ile Ser Asp Val Gly Thr Gln Thr  
 2295 1795 1800 1805  
 2297 Lys Ala Ile Asp Ser Thr Tyr Ala Thr Val Gly Met Pro Lys Ala Asn  
 2298 1810 1815 1820  
 2300 Ala Val Asn Leu Ile Gly Gln Asn Gly Leu Gly Ser Ile Tyr His Ser  
 E--> 2301 825 1830 1835 1840  
 2303 Pro Asp Ser Ala Tyr Lys Thr Trp Gln Leu Leu Asp Gln Phe Ala Asn  
 2304 1845 1850 1855  
 2306 Lys Gly Gly Asp Ala Val Phe Leu Arg Pro Ala Thr Glu Met Lys Cys  
 2307 1860 1865 1870  
 2309 Ala Gly Ala Pro Leu Lys Tyr Thr Phe Ile Val Arg Asp Tyr Leu Leu  
 2310 1875 1880 1885  
 2312 Arg Arg His Thr Leu Asp Lys Ser Arg Leu Phe Tyr Asn Ala His Asn  
 2313 1890 1895 1900  
 2315 Lys Thr Leu Phe Ser Val Pro Ile Val Asp Ala Lys Val Lys Met Leu  
 E--> 2316 905 1910 1915 1920  
 2318 Phe Ala Glu Lys Asn Ile Gln Val Asn Tyr Asp Arg Ser Leu Thr Ala  
 2319 1925 1930 1935  
 2321 Ile Asp Leu Ser Lys Arg Ile Ala Thr Phe Asn Ser Pro Glu Gly Val  
 2322 1940 1945 1950  
 2324 Val Glu Val Pro Tyr Asp Phe Ile Asn Val Val Pro Pro Met Arg Ala  
 2325 1955 1960 1965  
 2327 Pro Asp Ala Val Arg Gln Ser Ala Leu Ala Trp Gln Glu Gly Lys Trp  
 2328 1970 1975 1980  
 2330 Ala Asn Asp Gly Trp Val Glu Val Glu Lys His Thr Leu Arg His Arg  
 E--> 2331 985 1990 1995 2000  
 2333 Arg Tyr Ala Asn Val Phe Ala Val Gly Asp Val Ala Gly Val Pro Lys  
 2334 2005 2010 2015  
 2336 Gly Lys Thr Ala Ala Ser Val Lys Trp Gln Val Pro Val Ala Val Ala  
 2337 2020 2025 2030  
 2339 His Leu Leu Ala Glu Leu Glu Gly Lys Pro Cys Asp Glu Ile Tyr Asn  
 2340 2035 2040 2045  
 2342 Gly Tyr Thr Ser Cys Pro Leu Ile Thr Gln Leu Gly Lys Gly Met Leu  
 2343 2050 2055 2060  
 2345 Val Glu Phe Asp Tyr Asn Asn His Leu Thr Pro Ser Phe Pro Gly Val  
 E--> 2346 065 2070 2075 2080  
 2348 Ile Ala Pro Leu Glu Glu Leu Trp Ala Thr Trp Ala Ile Lys Thr Leu  
 2349 2085 2090 2095  
 2351 Gly Leu Lys Pro Thr Tyr Leu Gly Met Leu Arg Gly Leu Ala  
 2352 2100 2105 2110  
 3855 <210> SEQ ID NO: 28  
 3856 <211> LENGTH: 450  
 3857 <212> TYPE: PRT  
 3858 <213> ORGANISM: Pasteurella multocida  
 3860 <400> SEQUENCE: 28  
 3861 Ser Thr Lys Val Gly Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu  
 3862 1 5 10 15  
 3864 Phe Leu Glu Asp Arg Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu  
 3865 20 25 30

Same  
see p. 4

See next page

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```

3867 Gly Leu Ser Asp Ala Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu
3868          35          40          45
3870 Arg Tyr Gly Ile Glu Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr
3871          50          55          60
3873 Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu
3874          65          70          75          80
3876 Gln Glu Phe Asp Ile Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser
3877          85          90          95
3879 Phe Val Tyr Leu Gln Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr
3880          100         105         110
E--> 3882 Ser Pro Leu Tyr Trp Gly Pro Ser Arg His Arg Leu Xaa Ala Lys Phe
3883          115         120         125
E--> 3885 Glu Phe Arg Asp Xaa Phe Leu Glu Asn Met Asn Lys Xaa Phe Thr Phe
3886          130         135         140
E--> 3888 Arg Pro Trp Gln Ile Asn Xaa Phe Arg Gln Gln Gly Arg Asn Asn Tyr
3889          145         150         155         160
3891 Thr Glu Val Phe Pro Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met
3892          165         170         175
3894 Asp Asp Ile Lys Ile Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg
3895          180         185         190
3897 Trp Asp His Tyr Asn Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile
3898          195         200         205
3900 Asn Arg Thr Gln Arg Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser
3901          210         215         220
3903 Tyr Gln Leu Ser Leu Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala
3904          225         230         235         240
3906 Tyr Arg Leu Ser Thr Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr
3907          245         250         255
3909 Phe Glu Asp Arg Gly Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp
3910          260         265         270
3912 Leu Gln Pro Glu Thr Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln
3913          275         280         285
3915 Asn Gln Tyr Ala His Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His
3916          290         295         300
3918 Asn Phe Ile Gln Glu Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu
3919          305         310         315         320
3921 Tyr Asn Arg Thr Tyr Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe
3922          325         330         335
3924 Val Asn Glu Pro Glu Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala
3925          340         345         350
3927 Leu Asn Gly Ser Ala Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu
3928          355         360         365
3930 Lys Gly Ser Tyr Ser Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys
3931          370         375         380
3933 Ser Ile Gln Pro Trp Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu
3934          385         390         395         400
3936 Gly Trp Ser Val Ser Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala
3937          405         410         415
3939 Lys Asp Ala Ile Glu Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys

```

Sequence #28  
is missing the  
mandatory <220>  
to <223> features  
to explain the  
"Xaa's" in the  
sequence. see  
#9 on the  
Error Summary  
Sheet.



## RAW SEQUENCE LISTING

DATE: 06/27/2001

PATENT APPLICATION: US/09/545,199B

TIME: 12:40:15

Input Set : C:\Crf3\Datahold\09545199

Output Set: N:\CRF3\06262001\I545199B.raw

3940                    420                    425                    430  
 3942 Gln Trp Pro His Leu Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly  
 3943                    435                    440                    445  
 3945 Gln Val  
 3946                    450  
 5300 <210> SEQ ID NO: 36  
 5301 <211> LENGTH: 302  
 5302 <212> TYPE: PRT  
 5303 <213> ORGANISM: Pasteurella multocida  
 5305 <400> SEQUENCE: 36  
 5306 Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val  
 5307    1                    5                    10                    15  
 5309 Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe  
 5310                    20                    25                    30  
 5312 Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn  
 5313                    35                    40                    45  
 5315 Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn  
 5316                    50                    55                    60  
 5318 Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu  
 5319    65                    70                    75                    80  
 5321 Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu  
 5322                    85                    90                    95  
 5324 Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu  
 5325                    100                    105                    110  
 5327 Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys  
 5328                    115                    120                    125  
 5330 Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile  
 5331                    130                    135                    140  
 5333 Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe  
 5334    145                    150                    155                    160  
 5336 Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp  
 5337                    165                    170                    175  
 5339 Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile  
 5340                    180                    185                    190  
 5342 Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe  
 5343                    195                    200                    205  
 E--> 5345 Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Xaa Gln Tyr His Lys Gly  
 5346                    210                    215                    220  
 E--> 5348 Lys Xaa Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val  
 5349    225                    230                    235                    240  
 5351 Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys  
 5352                    245                    250                    255  
 E--> 5354 His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Xaa Xaa Ser Arg  
 5355                    260                    265                    270  
 E--> 5357 Gly Xaa Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala  
 5358                    275                    280                    285  
 5360 Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr  
 5361                    290                    295                    300  
 5472 <210> SEQ ID NO: 38

missing <220> to <223> features  
 to explain "Xaa's" in the sequence.

## RAW SEQUENCE LISTING

DATE: 06/27/2001

PATENT APPLICATION: US/09/545,199B

TIME: 12:40:15

Input Set : C:\Crf3\Datahold\09545199

Output Set: N:\CRF3\06262001\I545199B.raw

5473 <211> LENGTH: 166  
 5474 <212> TYPE: PRT  
 5475 <213> ORGANISM: Pasteurella multocida  
 5477 <400> SEQUENCE: 38

*missing <220> to <223> features for "Xaa's"*

5478 Leu Asn Lys Ala Gly Lys Ile Gln Tyr Val Leu Leu Lys Gly Asn Gln  
 5479 1 5 10 15  
 5481 Gly His Pro Asp Ala Glu Ala Arg Thr Lys Phe Val Ile Lys Glu Leu  
 5482 20 25 30  
 E--> 5484 Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met  
 5485 35 40 45  
 5487 Trp Asp Ala Ala Leu Ala Lys Asp Lys Met Asp Ala Trp Leu Ser Ser  
 5488 50 55 60  
 5490 Ser Lys Ala Asn Gln Ile Glu Val Ile Ile Ala Asn Asn Asp Gly Met  
 5491 65 70 75 80  
 5493 Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro  
 5494 85 90 95  
 E--> 5496 Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys  
 5497 100 105 110  
 5499 Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys  
 5500 115 120 125  
 5502 Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr  
 5503 130 135 140  
 5505 Glu Gly Thr Lys Trp Gln Leu Lys Arg Ser Cys Pro Thr Tyr Pro Leu  
 5506 145 150 155 160  
 5508 Cys Trp Cys Gly Cys Gly  
 5509 165

*"Xaa" in sequence*  
*→ see p. 13*

11512 <210> SEQ ID NO: 103  
 11513 <211> LENGTH: 1643  
 11514 <212> TYPE: PRT  
 11515 <213> ORGANISM: Pasteurella multocida  
 11517 <400> SEQUENCE: 103

11518 Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Gln Val Lys Gly Cys  
 11519 1 5 10 15  
 11521 Leu Val Pro Val Ala Glu Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser  
 11522 20 25 30  
 11524 Ser Asp Ser Thr Ser Thr Ser Glu Gln Val Glu Glu Glu Pro Phe Leu  
 11525 35 40 45  
 11527 Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr  
 11528 50 55 60  
 11530 Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser  
 11531 65 70 75 80  
 11533 Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys  
 11534 85 90 95  
 11536 Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile  
 11537 100 105 110  
 11539 Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr  
 11540 115 120 125  
 11542 Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly  
 11543 130 135 140

## RAW SEQUENCE LISTING

DATE: 06/27/2001

PATENT APPLICATION: US/09/545,199B

TIME: 12:40:16

Input Set : C:\Crf3\Datahold\09545199

Output Set: N:\CRF3\06262001\I545199B.raw

```

11545 Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser
11546 145 150 155 160
11548 Ala Val Phe Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu
11549 165 170 175
11551 Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala
11552 180 185 190
11554 Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val
11555 195 200 205
11557 Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn
11558 210 215 220
11560 Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg
11561 225 230 235 240
11563 Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu
11564 245 250 255
11566 Lys Val Thr Lys Gly Asn Val Ile Ile Asp Ile Asp Gly Phe Ser Thr
11567 260 265 270
11569 Asp Gly Leu Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys
11570 275 280 285
11572 Gln Ser Ile Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr
11573 290 295 300
11575 Leu Ile Ala Gly Ser Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys
11576 305 310 315 320
11578 Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly
11579 325 330 335
11581 Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr
11582 340 345 350
11584 Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn
11585 355 360 365
11587 Asp Ile Gln Ile Glu Met Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr
11588 370 375 380
11590 Ile Gln Gln Thr Val Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys
11591 385 390 395 400
11593 Lys Ile Glu Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr
11594 405 410 415
11596 Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys
11597 420 425 430
11599 Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly
11600 435 440 445
11602 Ala Leu Ser Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp
11603 450 455 460
11605 Val Ala Thr Glu Thr Leu Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu
11606 465 470 475 480
11608 Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala
11609 485 490 495
11611 Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile
11612 500 505 510
11614 Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg
11615 515 520 525
11617 Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser

```

## RAW SEQUENCE LISTING

DATE: 06/27/2001

PATENT APPLICATION: US/09/545,199B

TIME: 12:40:16

Input Set : C:\Cr3\Outhold\09545199

Output Set: N:\CRF3\06262001\I545199B.raw

```

11618      530      535      540
11620 Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu
11621 545      550      555      560
11623 Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu
11624      565      570      575
11626 Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu Thr Ile Asn
11627      580      585      590
11629 Ala Gln Asn Ile Glu Ile Asp Lys Asn Gln Asp Ile Gln Leu Gly Ala
11630      595      600      605
11632 Asn Ile Thr Leu Asn Val Glu Glu Asn Phe Val Asn Arg Ala Gly Thr
11633      610      615      620
11635 Leu Ala Thr Gly Lys Thr Leu Thr Ile Asn Thr Glu Ser Gly Ser Ile
11636 625      630      635      640
11638 Tyr Asn Leu Gly Gly Thr Leu Gly Ala Gly Lys Ser Leu Lys Leu Thr
11639      645      650      655
11641 Ala Lys Ser Thr Glu Glu Gly Met Gly Asn Ile Val Asn Gln Glu Asn
11642      660      665      670
11644 Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser
11645      675      680      685
11647 Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr Val His
11648      690      695      700
11650 Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val Ser Tyr
11651 705      710      715      720
11653 Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val
11654      725      730      735
11656 His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu Gln Glu
11657      740      745      750
11659 Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile Arg Ser
11660      755      760      765
11662 Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser Glu Ser
11663      770      775      780
11665 Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe
11666 785      790      795      800
11668 Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe Asn Gln
11669      805      810      815
11671 Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr Met Tyr
11672      820      825      830
11674 Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly Asn Ala
11675      835      840      845
11677 Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala Leu Phe Gly
11678      850      855      860
11680 Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn Phe Ser
11681 865      870      875      880
11683 Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr Gln Lys
11684      885      890      895
11686 Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser Tyr Asp
11687      900      905      910
11689 Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr Asp Phe
11690      915      920      925

```

## RAW SEQUENCE LISTING

DATE: 06/27/2001

PATENT APPLICATION: US/09/545,199B

TIME: 12:40:16

Input Set : C:\Crf3\Datahold\09545199

Output Set: N:\CRF3\06262001\I545199B.raw

```

11692 Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys Leu Glu
11693      930      935      940
11695 Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys
11696 945      950      955      960
11698 Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu Pro Ser
11699      965      970      975
11701 Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu Glu Asp
11702      980      985      990
11704 Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu
11705      995      1000      1005
11707 Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu Ser Pro Ile
11708      1010      1015      1020
11710 Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu Glu Ser
11711 1025      1030      1035      1040
11713 His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp Glu Ser
11714      1045      1050      1055
11716 Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys Glu Met
11717      1060      1065      1070
11719 Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn Lys Pro
11720      1075      1080      1085
11722 Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe
11723      1090      1095      1100
11725 Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly Glu Glu
11726 1105      1110      1115      1120
11728 Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr Asn Leu
11729      1125      1130      1135
11731 Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg Glu Lys
11732      1140      1145      1150
11734 Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu Gln Glu
11735      1155      1160      1165
11737 Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys Ala Arg
11738      1170      1175      1180
11740 Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu Lys Arg Val
11741 1185      1190      1195      1200
11743 Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp Lys Ile Ala
11744      1205      1210      1215
11746 Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu Ile Arg
11747      1220      1225      1230
11749 Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Lys Lys
11750      1235      1240      1245
11752 Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln Ala Glu Gln
11753      1250      1255      1260
11755 Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu Asp Ile Glu
11756 1265      1270      1275      1280
11758 Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala Glu Ala Ser
11759      1285      1290      1295
11761 Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro Lys Val Glu
11762      1300      1305      1310
11764 Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln Asp Asp

```

## RAW SEQUENCE LISTING

DATE: 06/27/2001

PATENT APPLICATION: US/09/545,199B

TIME: 12:40:16

Input Set : C:\Crf3\Datahold\09545199

Output Set: N:\CRF3\06262001\I545199B.raw

```

11765      1315      1320      1325
11767 Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu Asn Thr Lys
11768      1330      1335      1340
11770 Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp His Gln
11771 1345      1350      1355      1360
11773 Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu Asn Gln
11774      1365      1370      1375
11776 Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met Asp Asn
11777      1380      1385      1390
11779 Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala Ala Leu
11780      1395      1400      1405
11782 Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp Tyr Val
11783      1410      1415      1420
11785 Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val Tyr Phe
11786 1425      1430      1435      1440
11788 Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly Leu Gly Thr
11789      1445      1450      1455
11791 Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp Val Val
11792      1460      1465      1470
11794 Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn
11795      1475      1480      1485
11797 Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu Thr Arg Leu
11798      1490      1495      1500
11800 Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala Asn Asp
11801 1505      1510      1515      1520
11803 Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu Gly His
11804      1525      1530      1535
11806 Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln Ala Ser
11807      1540      1545      1550
11809 Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp Val Asn Leu
11810      1555      1560      1565
11812 Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe Ser Pro
11813      1570      1575      1580
11815 Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys Val Pro
11816 1585      1590      1595      1600
11818 Leu Leu Gly Val Ser Val Ser Ile Gln Phe Ile Gln Ser Ile Leu Val
11819      1605      1610      1615
E--> 11821 Arg Gln Leu Gln Glu Gly Ser Ile Phe Glu Val Gly His Leu His Xaa
11822      1620      1625      1630
11824 Ala Val Asp Arg Arg Cys Glu Pro Ser Gly Glu
11825      1635      1640

```

Xaa in  
sequence.  
needs <220>  
to <223> features.

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p. 14

<210> SEQ ID NO 1  
 <211> LENGTH: 1112  
 <212> TYPE: DNA  
 <213> ORGANISM: Pasteurella multocida  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (210)..(1001)  
 <223> OTHER INFORMATION: atpB  
 <400> SEQUENCE: 1

*missing mandatory <220> to <223>  
 features to explain the "n"  
 at position 1104 in the  
 sequence.*

```

gtcaacaaca ttttatggtg gagaggccgt taaatttata tccacaattt ttttgattgt 60
acttgctttt aaactgttca attcaatgca ttttattgca ttttttggtg gatattttat 120
aacaatagtt ttaaacaata ttcttccatt ttttataagt aagtacttaa atataaagca 180
ttttcataaa tatcaataaa ggattagtt atg gca gca gag ctt aca aca gcg 233
                               1       5
                               Met Ala Ala Glu Leu Thr Thr Ala
gga tat att ggg cac cat tta gca ttc ttg aaa aca ggg gat tct ttc 281
Gly Tyr Ile Gly His His Leu Ala Phe Leu Lys Thr Gly Asp Ser Phe
   10       15       20
tgg cat gtt cat tta gat acc ctt cta ttt tca att att tca ggt gca 329
Trp His Val His Leu Asp Thr Leu Leu Phe Ser Ile Ile Ser Gly Ala
   25       30       35       40
att ttt ctt ttt gtt ttt tca aaa gtt gca aaa aaa gca acg ccg ggt 377
Ile Phe Leu Phe Val Phe Ser Lys Val Ala Lys Lys Ala Thr Pro Gly
           45       50       55
gtg cct agc aag atg caa tgt ttt gtt gag ata atg gtt gat tgg att 425
Val Pro Ser Lys Met Gln Cys Phe Val Glu Ile Met Val Asp Trp Ile
           60       65       70
gat ggg atc gta aaa gaa aat ttc cat ggt cct cgt cat gct gtt gga 473
Asp Gly Ile Val Lys Glu Asn Phe His Gly Pro Arg His Ala Val Gly
           75       80       85
cca tta gca tta act att ttc tgc tgg gta ttc att atg aat gct atc 521
Pro Leu Ala Leu Thr Ile Phe Cys Trp Val Phe Ile Met Asn Ala Ile
           90       95       100
gat ttg atc cca gta gat ttc cta cct caa tta gcc cat tta ttt ggt 569
Asp Leu Ile Pro Val Asp Phe Leu Pro Gln Leu Ala His Leu Phe Gly
       105       110       115       120
att gaa tac tta aga gct gtt cca aca gca gat atc agt gga aca tta 617
Ile Glu Tyr Leu Arg Ala Val Pro Thr Ala Asp Ile Ser Gly Thr Leu
           125       130       135
ggc tta tca att ggt gtc ttc ttc tta att att ttc tat aca atc aaa 665
Gly Leu Ser Ile Gly Val Phe Phe Leu Ile Ile Phe Tyr Thr Ile Lys
           140       145       150
tca aaa ggt atg agt ggc ttt gtt aaa gaa tat acg ctt cat cct ttt 713
Ser Lys Gly Met Ser Gly Phe Val Lys Glu Tyr Thr Leu His Pro Phe
           155       160       165
aat cat cct ttg tta att ccg gtt aac tta gcg ctt gaa tca gtc aca 761
Asn His Pro Leu Leu Ile Pro Val Asn Leu Ala Leu Glu Ser Val Thr
           170       175       180
tta tta gca aaa cct gtt tct ttg gcg ttc cgt ctt ttc ggg aat atg 809
Leu Leu Ala Lys Pro Val Ser Leu Ala Phe Arg Leu Phe Gly Asn Met
       185       190       195       200
tat gca ggt gaa ctt atc ttt att ctt att gca gtg atg tac atg gca 857
Tyr Ala Gly Glu Leu Ile Phe Ile Leu Ile Ala Val Met Tyr Met Ala
           205       210       215
aat aat ttt gca ctt aat tca atg ggt att ttc atg cat ttg gct tgg 905
Asn Asn Phe Ala Leu Asn Ser Met Gly Ile Phe Met His Leu Ala Trp
           220       225       230

```

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gct att ttc cat att ctt gtg att acc tta' caa gca ttt att ttt atg	953
Ala Ile Phe His Ile Leu Val Ile Thr Leu Gln Ala Phe Ile Phe Met	
235 240 245	
atg ctt aca gtg gtt tat ttg agt atg ggt tat aac aaa gca gaa cac	1001
Met Leu Thr Val Val Tyr Leu Ser Met Gly Tyr Asn Lys Ala Glu His	
250 255 260	
taatttttta taaacaaaac cagaccttgg gtctaaattt caatcttatg gagaacatta	1061
tggaacactg taattactac aacaatcatc gcatctgnaa t <sup>Ⓢ</sup> ttcttgc t	1112

F.Y.I. →

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Note: see verification summary on pages 16 and 17 of this listing to see which sequences need "n" or "Xaa" explanations



## VERIFICATION SUMMARY

DATE: 06/27/2001

PATENT APPLICATION: US/09/545,199B

TIME: 12:40:17

Input Set : C:\Crf3\Datahold\09545199

Output Set: N:\CRF3\06262001\I545199B.raw

L:2 M:270 C: Current Application Number differs, Replaced Current Application No  
L:2 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:2 M:289 W: Identifier Missing or Out-Of-Order, <150> PRIOR APP NO  
L:0 M:201 W: Mandatory field data missing, APPLICANT NAME  
L:0 M:201 W: Mandatory field data missing, TITLE INVENTION  
L:0 M:201 W: Mandatory field data missing, FILE REFERENCE  
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:2151 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16  
L:2166 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16  
L:2181 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16  
L:2196 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16  
L:2211 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16  
L:2226 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16  
L:2241 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16  
L:2256 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16  
L:2271 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16  
L:2286 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16  
L:2301 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16  
L:2316 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16  
L:2331 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16  
L:2346 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16  
L:3766 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:3767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:3770 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:3771 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:3774 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:3775 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:3882 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28  
L:3885 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28 ✓  
L:3888 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28  
L:5261 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35  
L:5262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35  
L:5273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35  
L:5274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35  
L:5289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35  
L:5297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35  
L:5345 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:36  
L:5348 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:36 ✓  
L:5354 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:36  
L:5357 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:36  
L:5385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:5386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:5401 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:5402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:5433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:5435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:5461 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:5463 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37

## VERIFICATION SUMMARY

DATE: 06/27/2001

PATENT APPLICATION: US/09/545,199B

TIME: 12:40:17

Input Set : C:\Crf3\Datahold\09545199

Output Set: N:\CRF3\06262001\I545199B.raw

L:5484 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:38 ✓  
L:5496 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:38  
L:5609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39  
L:6532 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47  
L:9085 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72  
L:10782 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:90  
L:10782 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:90  
L:10782 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:90  
L:10784 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:90  
L:10784 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:90  
L:10784 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:90  
L:11503 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:102  
L:11504 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:102  
L:11821 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:103 ✓